

A copy of the amended abstract of the disclosure marked to show changes is provided in Exhibit C.

To the claims:

Please delete claims 32, 60, 62, 68, 74 and 75.

Please amend the claims as follows:

D<sup>2</sup>  
9. (four times amended) A polypeptide with at least 30% sequence identity to the polypeptide of Seq. ID No. 2 and comprising greater than fifty amino acids in length and modified in order to have a composition selected from one of the following: at least 5-15 mole % methionine, at least 6-25 mole % threonine, and at least 4-9 mole % tryptophan; wherein the % sequence identity is based on the entire sequence and is determined by BLAST 2.0 using default parameters.

D<sup>3</sup>  
12. (Twice amended) The polypeptide of Claim 10 wherein the protein exhibits reduced inhibitory activity against chymotrypsin, subtilisin or elastase when compared with the inhibitory activity against chymotrypsin, subtilisin or elastase exhibited by Seq. ID No. 4.

D<sup>4</sup>  
14. (Twice amended) The polypeptide of claim 10, further comprising one of the following pairs of substitutions: T22C and V82C; or E23C and R81C.

D<sup>5</sup>  
18. (three times amended) The polypeptide of Claim 15 wherein the amino-terminal extension comprises at least one to eighteen additional residues corresponding to amino acid residues 1 to 18 of Seq. ID No. 2 or 12.

19. (three times amended) A polypeptide comprising Seq. ID No. 2 modified to contain two or more modifications, said two or more modifications corresponding to positions in Seq. ID No. 2 selected from the group consisting of:

D<sup>3</sup>  
H18A, H18I, H18L, H18V, H18M, N19K, N19T, L20M, L20I, L20V, E23T, E23K, S31T, S32K, E34K, E34T, V38M, V38I, V38L, L40M, L40I, L40V, Q41K, Q41T, Q47K, Q47T, I49M, I49I, I49L, I49V, I56K, I56T, M59G, R62K, R62T, I63M, I63L, I63V, R65K, R65T, R67K, R67T, F69W, L73K, L73T, N75K, N75T, Q78K, Q78T, V79T, V79K, R81K, and R81T; and

further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

21. (three times amended) A polypeptide comprising Seq. ID No. 2 modified to contain two or more modifications, said two or more modifications corresponding to positions in Seq. ID No. 2 selected from the group consisting of:

D<sup>6</sup>  
H18A, H18M, N19K, L20M, T22C, E23T, E23C, S31T, E34K, V38M, L40M, Q41K, Q47K, I49M, I56K, M59G, R62K, I63M, R65K, R67K, F69W, L73K, N75K, Q78K, V79T, R81K, R81C, and V82C; and

further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

T<sup>7</sup>  
28. (three times amended) A polypeptide comprising Seq. ID No. 2 modified to contain three or more modifications, said three or more modifications comprising non-native essential amino acids replacing native amino acids at positions corresponding to Seq. ID No. 2 and selected from the group consisting of positions

1, 8, 11, 17, 18, 19, 20, 22, 23, 31, 32, 34, 38, 40, 41, 45, 47, 49, 56, 58, 59, 60, 61, 62, 63, 64, 65, 67, 69, 73, 74, 75, 76, 77, 78, 79, 81 and 82; and excluding V and W at position 56; K, V and W at position 58; W, V

and K at position 59; T, I and K at position 60; V and W at position 61 and V and F at position 62; and further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

29. (three times amended) An isolated polypeptide comprising Seq. ID No. 6, 8, 10, 12, 14, 16, 18, 20 or a conservative substitution thereof, wherein said polypeptide or conservative substitution thereof has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters

30. (three times amended) An isolated polypeptide comprising at least twenty three contiguous amino acids of Seq. ID Nos. 6, 8, 10, 12, 14, 16, 18 or 20, wherein said polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

31. (three times amended) An isolated polypeptide with more than 79% sequence identity to the polypeptide of Seq. ID No. 20, wherein the percent sequence identity is determined by GAP analysis using Gap Weight of 12 and Length Weight of 4.

59. (three times amended) An isolated polypeptide with at least 60% sequence identity to the polypeptide of Seq. ID No. 2 comprising greater than fifty amino acids in length and comprising more than ten lysine amino acid residues.

61. (twice amended) An isolated polypeptide comprising Seq. ID Nos. 6, 8, 10, 12, 14, 16, 18 or 20.

63. (once amended) The polypeptide of claim 72, wherein the non-native essential amino acids are isoleucine, lysine, tryptophan, methionine, threonine, or mixtures thereof.

64. (once amended) The polypeptide of claim 72, wherein the non-native essential amino acids are lysine.

65. (once amended) The polypeptide of claim 72, further comprising an amino terminal extension.

69. (twice amended) The polypeptide of claim 72, wherein the non-native disulfide bond is with a non-native cysteine at one or more positions corresponding to Seq. ID No. 4 positions 23, 81, 22, 82, 53 or 70.

70. (once amended) The polypeptide of claim 72, further comprising at least two non-native cysteines.

72. (twice amended) A polypeptide comprising Seq. ID No. 4, wherein said polypeptide has been modified to contain at least one non-native disulfide bond and more than four non-native essential amino acids, and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 4, the percent sequence identity determined by Blast 2.0 using default parameters.

76. (twice amended) A polypeptide comprising Seq. ID No. 4, wherein said polypeptide has been modified to contain at least eleven non-native essential amino acids, and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 4, the percent sequence identity determined by Blast 2.0 using default parameters.

78. (twice amended) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 2 and modified to contain a non-native disulfide bond.

79. (twice amended) A polypeptide having at least 80% identity to the polypeptide of Seq. ID No. 6 and modified to contain a non-native disulfide bond.

80. (twice amended) The polypeptide of claim 79, having at least 90% sequence identity to the polypeptide of Seq. ID No. 6.

81. (twice amended) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 8 and modified to contain a non-native disulfide bond.

82. (twice amended) The polypeptide of claim 81, having at least 90% sequence identity to the polypeptide of Seq. ID No. 8.

83. (twice amended) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 10 and modified to comprise a non-native disulfide bond.

84. (twice amended) The polypeptide of claim 83, having at least 90% sequence identity to the polypeptide of Seq. ID No. 10.

87. (twice amended) A polypeptide comprising any one of Seq. ID Nos 35-53, wherein the polypeptide is modified to have a non-native disulfide bond and more than seven non-native essential amino acid residues, and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 2 as determined by Blast 2.0 using default parameters.

98. (new) A polypeptide with at least 30% sequence identity to the polypeptide of Seq. ID No. 2 and comprising greater than fifty amino acids in length and